WEST Search History

DATE: Wednesday, July 30, 2003

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB; PLUR=YES; OP=ADJ			
L2	L1 and env	41	L2
L1	HIV and Group O	481	L1

END OF SEARCH HISTORY

? b 155
07nov01 15:15:53 User208669 Session D1928.1
$0.26 0.073 DialUnits File1
$0.26 Estimated cost File1
$0.26 Estimated cost this search
$0.26 Estimated total session cost 0.073 DialUnits

File 155:MEDLINE(R) 1966-2001/Dec W1
*File 155: From 11/5/2001 the NLM will not update Medline until early 2002
This is the period in which the NLM completes the annual re-indexing.

Set Items Description
--- ----- -----------
? s hiv and o
98428 HIV
183980 O
S1 1316 HIV AND O
? s env and s1
5962 ENV
1316 S1
S2 105 ENV AND S1
? s py<1998
Processing
S3 9572908 PY<1998
? s s2 and s3
105 S2
9572908 S3
S4 49 S2 AND S3
? t s4/7/3 4 6 10 11 14 15 20 22 28

4/7/3
DIALOG(R)File 155:MEDLINE(R)
09582738 97418745 PMID: 9274821
Diversity of the immunodominant epitope of gp41 of HIV-1 subtype O and its validity for antibody detection.
Eberle J; Loussert-Ajaka I; Brust S; Zekeng L; Hauser PH; Kaptue L; Knapp S; Damond F; Saragosti S; Simon F; Gurtler LG
Pettenkofer Institute, University of Munchen, Germany.
Journal of virological methods (NETHERLANDS) Aug 1997, 67 (1) p85-91 , ISSN 0166-0934 Journal Code: HQR
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
The immunodominant regions of the gp41 from 13 HIV-1 subtype O strains from Cameroon, 11 from France and one from Germany were sequenced. The amino acid sequences were compared to those of the 3 published HIV-1 subtype O isolates, ANT70, MVP-5180 and VAU. All HIV-1 subtype O isolates had a very conserved amino acid sequence in this region and showed a subtype O specific structure. Within the cysteine loop there was a positive charge of two basic amino acids, arginine and lysine. Only two strains (CM.6778 and CM.8161) showed an acidic amino acid in this loop. None of the isolates showed the same amino acid sequence in this immunodominant region. A 25 residue peptide from the immunodominant domain of gp41 of the MVP-5180 strain was synthesized, cycled to form the cysteine-loop and coated to microtiter plates. Antibody binding was detected by indirect ELISA using an enzyme labeled anti-human IgG. Out of 111 anti-HIV-1 positive specimens, collected mainly from Cameroonian HIV infected patients, only 10 were not reactive in this assay. The 42 anti-HIV-1 subtype O positive specimens gave all a reaction above cut off. Despite the diversity found in the amino acid sequences within the 25 isolates a peptide-based indirect ELISA representing the immunodominant epitope of the strain MVP-5180 successfully detected all the anti-HIV-O sera so far tested, pointing to the importance of adding such a peptide for correct identification of HIV-1 subtype O infected patients, while some assays without HIV-O specific antigens partially fail to detect all anti-HIV-O specimens.
Record Date Created: 19971014

4/7/4
DIALOG(R)File 155:MEDLINE(R)
09579851 97407537 PMID: 9264286
Envelope sequence variability and serologic characterization of HIV type 1 group O isolates from equatorial guinea.
Hunt JC; Golden AM; Lund JK; Gurtler LG; Zekeng L; Obiang J; Kaptue L; Hampl H; Vallari A; Devare SG
AIDS Research and Retrovirus Discovery, Abbott Laboratories, North Chicago, Illinois 60064, USA.
AIDS research and human retroviruses (UNITED STATES) Aug 10 1997, 13 (12) p995-1005, ISSN 0889-2229 Journal Code: ART
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Four sera from Equatorial Guinea (EG) suspected to contain antibody against HIV-1 group O-related viruses were identified on the basis of unusual and differential serologic reactivity in selected commercial assays and Western blot. Degenerate primers, designed from HIV-1 group O published sequences, were used to PCR amplify envelope (env) gene sequences from the suspect EG sera. A complete envelope gene sequence from each serum was determined from the overlapping env gene fragments. Analysis (PHYLIP package of programs) of Env amino acid sequences (translated from nucleotide sequences) indicated that the amino acid sequences obtained from EG sera clustered more closely with HIV Env sequences of group O compared to group M. The amino acid sequences at the octameric tip of the V3 loop were either RIGPLAWY (one isolate), RIGPMAWY (two isolates), or GLGPLAVY (one isolate). The V3 tip tetrameric sequence GPLA is represented only once

in the 1995 HIV (Los Alamos) database, but was present in two of our group O-related EG samples. The gp41 immunodominant regions (IDR) protein sequences were identical for sequences from three of the sera, RLLALETLIQNQQLLNLWGCKGR(K)L(I)VCYTSVK(T)W, whereas sequence from the fourth
serum contained three changes as noted in parentheses. IDR sequences derived from EG sera were unique compared to those reported for other HIV-1 group O isolate ANT70, VAU, or MVP5180. Antibody in each EG serum directed against the IDR could be detected using synthetic peptides comprising sequences from the ANT70 or MVP5180 IDRs, but were most reactive against the sequences derived from the samples themselves. Little or no serologic reactivity was detected when EG sera were reacted against peptides comprising the IDR of HIV-1 group M (subtype B consensus) or HIV-2 (consensus).
Record Date Created: 19971010

4/7/6
DIALOG(R)File 155:MEDLINE(R)
09374592 97353064 PMID: 9209322
Molecular analyses of HIV-1 group O and HIV-2 variants from Africa.
Hunt JC; Brennan CA; Golden AM; Yamaguchi J; Lund JK; Vallari AS; Hickman RK; Zekeng L; Gurtler LG; Hampl H; Kaptue L; Devare SG
Abbott Laboratories, North Chicago, IL-60064, USA.
Leukemia (ENGLAND) Apr 1997, 11 Suppl 3 p138-41, ISSN 0887-6924 Journal Code: LEU
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Genetic variation among HIV isolates creates challenges for their detection by serologic and genetic techniques. To characterize the sequence variation and its correlation to serologic diversity of HIV-1 Group O and HIV-2 isolates, samples were identified by differential reactivity in selected commercial and research assays. Analysis of sera from Equatorial Guinea (EG) led to identification of 4 HIV-1 Group O variants. Viral RNA, extracted from these samples was used to PCR amplify overlapping sequences of the entire envelope gene using multiple primer pairs. Sequence analysis indicated that the V3 loop nucleotide and protein sequences aligned more closely with HIVANT70 compared to other Group O sequences. The amino acid sequences at the octameric tip of the V3 loop were RIGPLAWY, RIGPMAWY, or GLGPLAVY. The tetrameric tip GPLA is represented only once in the published 1994 HIV database (Los Alamos) but was present in 2 of 4 of EG samples. The immuno-dominant region (IDR) sequences derived from EG sera were unique in that none of the sequences were completely homologous to other HIV-1 group O variants. Further, the HIV-1 group O sequence variation could be correlated with differential serologic reactivity using IDR peptides. Compared to HIV-1, the sequence information on HIV-2 isolates is relatively limited, though the HIV-2 isolates also show genetic variation similar to HIV-1. To further establish a correlation between the genetic diversity and serologic detection of HIV-2, plasma samples from Western Africa were evaluated. Eight samples were selected based on weak serologic reactivity to env proteins. PCR amplification and sequence analysis of the gag, env V3 loop, and env IDR regions indicated that the samples could be classified as subtypes A (4 samples), B (3 samples) and D (1 sample). Across the subtypes, there was conservation in the IDR region of the sequence WGCAFRQVCHT. This region is absolutely conserved among the majority of currently known HIV-2 and related SIV viruses (1994 HIV database). One subtype B sample had a unique sequence immediately adjacent to the IDR, however, this did not change the serologic detection using a HIV-2 IDR specific monoclonal antibody.
Record Date Created: 19970807

4/7/10
DIALOG(R)File 155:MEDLINE(R)
09129094 97102930 PMID: 8947302
Env gene characterization of the first HIV type 1 group O Spanish isolate.
Mas A; Quinones-Mateu E; Soriano V; Domingo E
Servicio de Enfermedades Infecciosas, Instituto de Salud Carlos III, Madrid, Spain.
AIDS research and human retroviruses (UNITED STATES) Nov 20 1996, 12 (17) p1647-9, ISSN 0889-2229 Journal Code: ART
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Record Date Created: 19970227

4/7/11
DIALOG(R)File 155:MEDLINE(R)
09129078 97068247 PMID: 8911575
V3 loop sequence analysis of seven HIV type 1 group O isolates phenotyped in peripheral blood mononuclear cells and MT-2 cells.
De Jong J; Simon F; Van der Groen G; Baan E; Saragosti S; Brun-Vezinet F; Goudsmit J
Department of Human Retrovirology, Academic Medical Centre, Amsterdam, The Netherlands.
AIDS research and human retroviruses (UNITED STATES) Nov 1 1996, 12 (16) p1503-7, ISSN 0889-2229 Journal Code: ART
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
HIV-1-infected individuals from which syncytium-inducing (SI) viruses are isolated most often progress more rapidly to AIDS than individuals carrying only non-syncytium-inducing (NSI) viruses. The syncytium-inducing capacity of virus isolates is commonly determined in conjunction to replication in

MT-2 cells. Comparison of HIV-1 env sequences and a site-directed mutagenesis study have indicated that the presence of a positively charged amino acid at position 11 or 25 in the V3 loop is minimally required for the SI capacity of HIV-1 subtype B viruses. Studies have also shown a similar correlation between positively charged signature amino acids in the V3 loop and syncytium formation in MT-2 cells for HIV-1 subtypes A, D, and E. In the present study virus phenotype was determined and compared to the V3 loop sequence of seven HIV-1 group O isolates. Three of the HIV-1 group O isolates showed the NSI/non-MT-2 tropic phenotype and two showed the SI/MT-2 tropic phenotype, whereas two isolates presented an uncommon NSI/MT-2 tropic phenotype. The V3 loop of the two SI/MT-2 tropic isolates had a high net positive charge and contained a positively charged amino acid at position 11 or 25. The V3 loop of the two NSI/MT-2 tropic isolates had a low net positive charge and contained a single positively charged amino acid at position 37.
Record Date Created: 19970224

4/7/14
DIALOG(R)File 155:MEDLINE(R)
08995326 96263682 PMID: 8924250
An efficient method for the rescue and analysis of functional HIV-1 env genes: evidence for recombination in the vicinity of the tat/rev splice site.
Douglas NW; Knight AI; Hayhurst A; Barrett WY; Kevany MJ; Daniels RS
Virology Division, National Institute of Medical Research, Mill Hill, London, UK.
AIDS (UNITED STATES) Jan 1996, 10 (1) p39-46, ISSN 0269-9370 Journal Code: AID
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
OBJECTIVE: To establish a robust procedure for the isolation and characterization of full-length expression-competent HIV-1 env genes directly from patient samples. DESIGN: HIV exists as a quasispecies which can be disturbed by in vitro culture, in which numerous members of the population are likely to be defective due to the high error rate of the viral reverse transcriptase. Defective viruses are unlikely to play a dominant role in disease progression. Since env gene translation products play major roles in the initiation and spread of infection we need to study genes with open reading frames. METHODS: A nested polymerase chain reaction (PCR) approach has been used to rescue intact (2.6 kb) env genes, which are cloned into a T7-promoter-containing vector. Expression of gp160 in CV-1 cells is detected by Western blot. Expression-competent clones are sequenced and resulting sequences used for phylogenetic studies. Translation products are analysed in relation to the known immunogenic structure of gp160. RESULTS: From random patient samples collected in London clinics, only HIV-1 subtype B was found. Two of the samples contained viruses with an additional pair of cysteine residues in their V1 regions. For samples collected in Uganda, HIV-1 subtypes A, D and an A/D recombinant were recovered. CONCLUSION: An effective procedure is described for the isolation of HIV-1 env genes directly from patient samples, which has worked for A, B and D subtypes to date. The PCR primers can be utilized with other subtypes with the possible exception of subtype O viruses. Phylogenetic analyses revealed the potential importance of a G/C-rich region near the tat/rev splice site as a site of recombination. The sequences and translation products generated may be more relevant to disease progression in vivo and vaccine formulations than those obtained from viruses selected in long-term culture.
Record Date Created: 19961031

4/7/15
DIALOG(R)File 155:MEDLINE(R)
08965294 96379548 PMID: 8800800
HIV-1 subtype O: epidemiology, pathogenesis, diagnosis, and perspectives of the evolution of HIV.
Gurtler LG; Zekeng L; Tsague JM; van Brunn A; Afane Ze E; Eberle J; Kaptue L
Max von Pettenkofer Institute for Hygiene and Medical Microbiology, University of Munich, Federal Republic of Germany.
Archives of virology. Supplementum (AUSTRIA) 1996, 11 p195-202, ISSN 0939-1983 Journal Code: BLI
Languages: ENGLISH
Document type: Journal Article; Review; Review, Tutorial
Record type: Completed
HIV-1 subtype O is a new HIV variant originating in the West-Central African region, with highest prevalences in countries such as Cameroon, Equatorial Guinea and Gabon. Detection of antibodies to HIV-1 subtype O can pose problems in unmodified ELISA tests, and confirmation of anti-HIV-1 subtype O in immunoblot may give false negative results in some specimens. Nucleic acid-based assays designed for HIV-1 detection do not amplify or detect sequences from HIV-1 subtype O. In their env sequences, HIV-1 subtype O strains show a higher heterogeneity than the classical HIV-1 subtypes, leading to the conclusion that HIV-1 subtype O has been introduced into the human population only recently. Further, unidentified subtypes are also likely to exist. (15 Refs.)
Record Date Created: 19960927

4/7/20
DIALOG(R)File 155:MEDLINE(R)
08736009 95256388 PMID: 7537751
Reactivity of five anti-HIV-1 subtype O specimens with six different anti-HIV screening ELISAs and three immunoblots.
Gurtler LG; Zekeng L; Simon F; Eberle J; Tsague JM; Kaptue L; Brust S; Knapp S
Max von Pettenkofer Institute, University of Munich, Germany.

Journal of virological methods (NETHERLANDS) Feb 1995, 51 (2-3) p177-83, ISSN 0166-0934 Journal Code: HQR
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Five anti-subtype O specimens were tested by anti-HIV-1/2 screening and confirmatory assays. They can be divided into three specimens, reactive with all ELISAs, independent of the nature of the antigen (recombinant proteins or peptides) and test configuration (indirect ELISA or double antigen/sandwich ELISA). One specimen was not detected by one peptide based ELISA. One specimen was only recognized by two ELISAs and should be considered as a marker sample for the weakness of currently used ELISAs with anti-subtype O. Three different immunoblot assays available commercially detected two of the specimens with a major binding of gp160 and other viral bands, especially the integrase and reverse transcriptase. Another two specimens lacked reactivity with glycoproteins almost completely, but showed some staining with the enzymes of HIV, and would most probably be interpreted as indeterminate. The fifth specimen, which was also missed by most of the ELISAs, had very faint staining of the gp160 and a very weak staining of p24, and would most probably be interpreted as negative. Adaption of currently available tests to anti-subtype O is needed for the future reliability of anti-HIV diagnostic reagents.
Record Date Created: 19950606
4/7/22
DIALOG(R)File 155:MEDLINE(R)
08575450 95363977 PMID: 7637010
Variability of human immunodeficiency virus type 1 group O strains isolated from Cameroonian patients living in France.
Loussert-Ajaka I; Chaix ML; Korber B; Letourneur F; Gomas E; Allen E; Ly TD; Brun-Vezinet F; Simon F; Saragosti S
Laboratoire de Virologie, Hopital Bichat-Claude Bernard, Paris, France.
Journal of virology (UNITED STATES) Sep 1995, 69 (9) p5640-9, ISSN 0022-538X Journal Code: KCV
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Human immunodeficiency virus type 1 (HIV-1) nucleotide sequences encoding p24Gag and the Env C2V3 region were obtained from seven patients who were selected on the basis of having paradoxical seronegativity on a subset of HIV enzyme-linked immunosorbent assay detection kits and having atypical Western blot (immunoblot) reactivity. Sequence analyses showed that all of these strains were more closely related to the recently described Cameroonian HIV isolates of group O (HIV-1 outlier) than to group M (HIV-1 major). All seven patients had Cameroonian origins but were living in France at the time the blood samples were taken. Characterization of a large number of group M strains has to date revealed eight distinct genetic subtypes (A to H). Genetic distances between sequences from available group O isolates were generally comparable to those observed in M intersubtype sequence comparisons, showing that the group O viruses are genetically very diverse. Analysis of sequences from these seven new viral strains, combined with the three previously characterized group O strains, revealed few discernable phylogenetic clustering patterns among the 10 patients' viral sequences. The level of diversity among group O sequences suggests that they may have a comparable (or greater) age than the M group sequences, although for unknown reasons, the latter group dispersed first and is the dominant lineage in the pandemic.
Record Date Created: 19950914
4/7/28
DIALOG(R)File 155:MEDLINE(R)
08289706 95065659 PMID: 7975221
Isolation and envelope sequence of a highly divergent HIV-1 isolate: definition of a new HIV-1 group.
Charneau P; Borman AM; Quillent C; Guetard D; Chamaret S; Cohen J; Remy G ; Montagnier L; Clavel F
CNRS URA 1157, Departement Sida et Retrovirus, Institut Pasteur, Paris, France.
Virology (UNITED STATES) Nov 15 1994, 205 (1) p247-53, ISSN 0042-6822 Journal Code: XEA
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
We report here the isolation and envelope sequence of a divergent HIV-1 isolate from a French woman with AIDS. This virus, HIV-1VAU, is closely related to the recently described Cameroonian viral isolates HIV-1ANT70 and HIV-1MVP5180, until now designated HIV-1 subtype O. Phylogenetic analysis reveals that the three viruses are equidistant from one another and that their mutual divergence is similar to what has been reported between the more conventional HIV-1 subtypes. Therefore, these three viruses could be included in a new viral group, HIV-1 group O (outgroup), distinct from the cluster of other HIV-1 isolates, which we will refer to as group M (Major group). The HIV-1 group O is currently emerging in western central Africa but its spread in Europe has already started.
Record Date Created: 19941206
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07nov01 15:25:09 User208669 Session D1928.2
$6.33 1.977 DialUnits File155
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$2.00 10 Type(s) in Format 7
$2.00 59 Types
$8.33 Estimated cost File155
$0.50 TYMNET
$8.83 Estimated cost this search
$9.09 Estimated total session cost 2.050 DialUnits
Logoff: level 01.10.01 D 15:25:09